

SEQUENCE LISTING
INS B22

(1) GENERAL INFORMATION:

- (i) APPLICANT: JOHNSON, EUGENE M
MILBRANDT, JEFFREY D
KOTZBAUER, PAUL T
LAMPE, PATRICIA A
KLEIN, ROBERT
DESAUVAGE, FRED
- (ii) TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
- (iii) NUMBER OF SEQUENCES: 239
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: HOWELL & HAVERKAMP, L.C.
 - (B) STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 - (C) CITY: ST. LOUIS
 - (D) STATE: MO
 - (E) COUNTRY: USA
 - (F) ZIP: 63105
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: HOLLAND, DONALD R.
 - (B) REGISTRATION NUMBER: 35,197
 - (C) REFERENCE/DOCKET NUMBER: 971486
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 314-727-5188
 - (B) TELEFAX: 314-727-6092

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Arg	Leu	Gly	Ala	Arg	Pro	Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg
1					5				10					15	
Val	Ser	Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Asp	Glu	Thr	Val	Leu	Phe
							20		25				30		

Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu
 35 40 45

Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val
 50 55 60

Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser
 65 70 75 80

Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala
 85 90 95

Arg Glu Cys Ala Cys Val
 100

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
 1 5 10 15

Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 20 25 30

Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
 35 40 45

Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
 50 55 60

His Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu
 65 70 75 80

Asp Val His Ser Arg Tyr His Thr Leu Gin Glu Leu Ser Ala Arg Glu
 85 90 95

Cys Ala Cys Val
 100

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Gly Ala Arg Pro Xaa Gly Leu Arg Glu Leu Glu Val Ser Val Ser
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /note= "SERINE OR CYSTEINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Cys Ala Gly Ala Xaa Glu Ala Ala Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 17
 - (D) OTHER INFORMATION: /note= "GLUTAMINE OR GLUTAMIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Xaa Val Glu Ala Lys Pro Cys Cys Gly Pro Thr Ala Tyr Glu Asp
 1 5 10 15

Xaa Val Ser Phe Leu Ser Val
20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr His Thr Leu Gln Glu Leu Ser Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15

Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30

Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80

Pro Gly Pro Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala
85 90 95

Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val
100 105 110

Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg
115 120 125

Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly
130 135 140

Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg
145 150 155 160

Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe
 165 170 175
 Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg
 180 185 190
 Glu Cys Ala Cys Val
 195

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser
 1 5 10 15
 Leu Leu Ser Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg
 20 25 30
 Leu Gly Pro Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp
 35 40 45
 Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
 50 55 60
 Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile
 65 70 75 80
 Pro Gly Pro Arg Arg Ala Gly Pro Arg Arg Arg Ala Arg Pro
 85 90 95
 Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu
 100 105 110
 Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys
 115 120 125
 Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg
 130 135 140
 Arg Leu Arg Gln Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His
 145 150 155 160
 Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp
 165 170 175
 Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys
 180 185 190
 Ala Cys Val
 195

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCAGCGGTTGG	GGGCGCGGCC	TTGCGGGCTG	CGCGAGCTGG	AGGTGCGCGT	GAGCGAGCTG	60
GGCCTGGGCT	ACGCGTCCGA	CGAGACGGTG	CTGTTCCGCT	ACTGCGCAGG	CGCCTGCGAG	120
GCTGCCGCGC	GCGTCTACGA	CCTCGGGCTG	CGACGACTGC	GCCAGCGGCG	GCGCCTGCGG	180
CGGGAGCGGG	TGCGCGCGA	GCCCTGCTGC	CGCCCGACGG	CCTACGAGGA	CGAGGTGTCC	240
TTCCCTGGACG	CGCACAGCG	CTACCAACAG	GTGCACGAGC	TGTCGGCGCG	CGAGTGCGCC	300
TGCCTG						306

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGGGGCTC	GGCCTTGCTGG	GCTGCGCGAG	CTCGAGGTGC	GCGTGAGCGA	GCTGGGCCTG	60
GGCTACACGT	CGGATGAGAC	CGTGCTGTTG	CGCTACTGCG	CAGGCGCGTG	CGAGGCGGCC	120
ATCCGCATCT	ACGACCTGGG	CCTTCGGCGC	CTGCGCCAGC	GGAGGCGCGT	GCGCAGAGAG	180
CGGGCGCGGG	CGCACCCGTG	TTGTCGCCCG	ACGGCCTATG	AGGACGAGGT	GTCCTTCCTG	240
GACGTGCACA	GCCGCTACCA	CACCGCTGCAA	GAGCTGTCGG	CGCGGGAGTG	CGCGTGCCTG	300

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGCAGCGCT	GGAAGGCGGC	GGCCTTGGCC	TCAGTGCCTCT	GCAGCTCCGT	GCTGTCCATC	60
TGGATGTGTC	GAGAGGCCT	GCTTCTCAGC	CACCGCCCTCG	GACCTGCGCT	GGTCCCCCTG	120
CACCGCCTGC	CTCGAACCCCT	GGACGCCCGG	ATTGCCCGCC	TGGCCCAGTA	CCGTGCACTC	180

CTGCAGGGGG	CCCCGGATGC	GATGGAGCTG	CGCGAGCTGA	CGCCCTGGC	TGGGCGGCC	240
CCAGGTCCGC	GCCGTCGGC	GGGGCCCCGG	CGGC GGCGCG	CGCGTGC	GCG GTGGGGCG	300
CGGCCTTGC	GGCTGCGC	GAG GAGGTG	CGCGT GAGCG	AGCTGGGC	CCT GGGCTACCGC	360
TCCGACGAGA	CGGTGCTGTT	CCGCTACTGC	GCAGGCGCCT	GCGAGGCTGC	CGCGCGCGTC	420
TACGACCTCG	GGCTGCGACG	ACTGCGCCAG	CGGC GGCGCC	TGCGGCGGGA	GC GG GTGC	480
GCGCAGCCCT	GCTGCCGCC	GACGGCCTAC	GAGGACGAGG	TGTCCTTCCT	GGACGCGCAC	540
AGCCGCTACC	ACACGGTGG	CGAGCTGTCG	GCGCGCGAGT	GCGCCTGCGT	G	591

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAGGGCGCT	GGAAGGCAGC	GGCCCTGGTG	TCGCTCATCT	GCAGCTCCCT	GCTATCTGTC	60
TGGATGTGCC	AGGAGGGTCT	GCTCTTGGC	CACCGCCTGG	GACCCGCGCT	TGCCCCGCTA	120
CGACGCCCTC	CACGCACCC	GGACGCCCGC	ATCGCCGCC	TGGCCCAGTA	TCGCGCTCTG	180
CTCCAGGGCG	CCCCCGACGC	GGTGGAGCTT	CGAGAACTTT	CTCCCTGGC	TGCCCCGATC	240
CCGGGACCGC	GCCGTCGAGC	GGGTCCCCGG	CGTCGGCGGG	CGCCGCCGGG	GGCTCGGCCT	300
TGTGGGCTGC	GCGAGCTCGA	GGTGCGCGT	AGCGAGCTGG	GCCTGGCTA	CACGTCGGAT	360
GAGACCGTGC	TGTTCCGCTA	CTGCGCAGGC	CGCGTGCAGG	CGGCCATCCG	CATCTACGAC	420
CTGGGCCTTC	GGCGCCTGCG	CCAGCGGAGG	CGCGTGC	GAGAGCGGGC	GCGGGCGCAC	480
CCGTGTTGTC	GCCCGACGGC	CTATGAGGAC	GAGGTGTCCT	TCCTGGACGT	GCACAGCCGC	540
TACCACACGC	TGCAAGAGCT	GTCGGCGCGG	GAGTGCGCGT	GCGT	G	585

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGGGAGAG	CGCGCGGTGG	TTTCGTCCGT	GTGCCCCGCG	CCC CGCGCTC	CTCGCGTGGC	60
CCCGCGTCCT	GAGCGCGCTC	CAGCCTCCCA	CGCGCGCCAC	CCC GGGGTTTC	ACTGAGCCCG	120

GCGAGCCGG	GGAAGACAGA GAAAGAGAGG CCAGGGGGG AACCCATGG CCCGGCCCGT	180
GTCCCGCACC	CTGTGCCTTG GCCTCCTCCG GCACGGGTC CCCGGTCGC CTCCGGTCCC	240
CGCGATCCGG	ATGGCGCACG CAGTGGCTGG GGCGGGCCG GGCTCGGGTG GTCGGAGGAG	300
TCACCACTGA	CCGGGTCAATC TGGAGCCCGT GGCAGGCCGA GGCCCAGG	348

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTACCTCA CGCCCCCGA CCTGCGAAAG GGCCCTCCCT GCCGACCCCTC GCTGAGAACT	60
GACTTCACAT AAAGTGTGGG AACTCCCC	87

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser	
1 5 10 15	
Val Leu Ser	

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser	
1 5 10 15	
Leu Leu Ser	

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCC

57

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGAGGCAGCT GGAAGGCAGC GGCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCT

57

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile	Trp	Met	Cys	Arg	Glu	Gly	Leu	Leu	Leu	Ser	His	Arg	Leu	Gly	Pro
1															15

Ala	Leu	Val	Pro	Leu	His	Arg	Leu	Pro	Arg	Thr	Leu	Asp	Ala	Arg	Ile
															30
20															

Ala	Arg	Leu	Ala	Gln	Tyr	Arg	Ala	Leu	Leu	Gln	Gly	Ala	Pro	Asp	Ala
															45
35															

Met	Glu	Leu	Arg	Glu	Leu	Thr	Pro	Trp	Ala	Gly	Arg	Pro	Pro	Gly	Pro
															60
50															

Arg	Arg	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Arg	Ala	Arg				
65															
70															
75															

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTGGATGT GTCGAGAGGG CCTGCTTCTC AGCCACCGCC TCGGACCTGC GCTGGTCCCC	60
CTGCACCGCC TGCCTCGAAC CCTGGACGCC CGGATTGCC GCCTGGCCCA GTACCGTGCA	120
CTCCTGCAGG GGGCCCCCGA TGCGATGGAG CTGCGCGAGC TGACGCCCTG GGCTGGGCGG	180
CCCCCAGGTC CGCGCCGTCG GGCGGGGCC CGGCGGCCGG CCGCGCGT	228

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTCTGGATGT GCCAGGAGGG TCTGCTTTG GGCCACCGCC TGGGACCCGC GCTTGCCCCG	60
CTACGACGCC CTCCACGCAC CCTGGACGCC CGCATGCC GCCTGGCCCA GTATCGCGCT	120
CTGCTCCAGG GCGCCCCCGA CGCGGTGAG CTTCGAGAAC TTTCTCCCTG GGCTGCCCGC	180
ATCCCAGGAC CGCGCCGTCG AGCGGGTCCC CGGCGTCGGC GGGCGCGG	228

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg Leu Gly Pro	
1 5 10 15	
Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp Ala Arg Ile	
20 25 30	
Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala Pro Asp Ala	
35 40 45	
Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile Pro Gly Pro	
50 55 60	

Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15

Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30

Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80

Pro Gly Pro Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
85 90 95

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser
1 5 10 15

Leu Leu Ser Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg
20 25 30

Leu Gly Pro Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile
65 70 75 80

Pro Gly Pro Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
85 90 95

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGCAGCGCT GGAAGGCGGC GGCCCTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC	60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG	120
CACCGCCTGC CTCGAACCCCT GGACGCCCGG ATTGCCGCC TGGCCCAGTA CCGTGCACTC	180
CTGCAGGGGG CCCCGGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGCCC	240
CCAGGTCCGC GCCGTCGGGC GGGGCCCGG CGGCAGCGCG CGCGT	285

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGAGGGCCT GGAAGGCAGC GGCCCTGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCCT GGACGCCCGG ATCGGCCGCC TGGCCCAGTA TCGCGCTCTG	180
CTCCAGGGCG CCCCGACGC GGTGGAGCTT CGAGAACTTT CTCCCTGGGC TGCCCGCCTC	240
CCGGGACCGC GCCGTCGAGC GGGTCCCCGG CGTCGGCGGG CGCGG	285

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCAGCGCT GGAAGGCGGC GGCCCTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC	60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG	120

CACCGCCTGC CTCGAACCCT GGACGCCCGG ATTGCCCGCC TGGCCCAGT 169

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACCGTGCACT CCTGCAGGGG GCCCCGGATG CGATGGAGCT GCGCGAGCTG ACGCCCTGGG	60
CTGGGCGGCC CCCAGGTCCG CGCCGTCGGG CGGGGCCCCG GCGGCGGCGC GCGCGTGC	120
GGTTGGGGGC GCGGCCTTGC GGGCTGCGCG AGCTGGAGGT GCGCGTGAGC GAGCTGGGCC	180
TGGGCTACGC GTCCGACGAG ACGGTGCTGT TCCGCTACTG CGCAGGCGCC TGCGAGGCTG	240
CCGCGCGCGT CTACGACCTC GGGCTGCGAC GACTGCGCCA GCGGCAGCGC CTGCGGCGG	300
AGCGGGTGCG CGCGCAGCCC TGCTGCCGCC CGACGGCCTA CGAGGACGAG GTGTCCCTCC	360
TGGACGCGCA CAGCCGCTAC CACACGGTGC ACGAGCTGTC GGCACGCGAG TGCGCCTGCG	420
TGTGA	425

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGAGGCGCT GGAAGGCAGC GGGCCTGGTG TGGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCCT GGACGCCCGC ATCCCCGCC TGGCCCAGT	169

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATCGCGCTCT	GCTCCAGGGC	GCCCCGACG	CGGTGGAGCT	TCGAGAACTT	TCTCCCTGGG	60
CTGCCCGCAT	CCCGGGACCG	CGCCGTCGAG	CGGGTCCCCG	GCGTCGGCGG	GCGCGGCCGG	120
GGGCTCGGCC	TTGTGGGTG	CGCGAGCTCG	AGGTGCGCGT	GAGCGAGCTG	GGCCTGGGCT	180
ACACGTCGGA	TGAGACCGTG	CTGTTCCGCT	ACTGCGCAGG	CGCGTGCAG	GCGGCCATCC	240
GCATCTACGA	CCTGGGCCTT	CGGCGCCTGC	GCCAGCGGAG	GCGCGTGCAG	AGAGAGCGGG	300
CGCGGGCGCA	CCCGTGTGTT	CGCCCGACGG	CCTATGAGGA	CGAGGTGTCC	TTCCTGGACG	360
TGCACAGCCG	CTACCACACG	CTGCAAGAGC	TGTCGGCGCG	GGAGTGCAG	TGCGTGTGA	419

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1															15
Tyr	Ala	Ser	Asp	Glu	Thr	Val	Lys	Phe	Arg	Tyr	Cys	Ala	Gly	Ala	Cys
															30
Glu	Ala	Ala	Ala	Arg	Val	Tyr	Asp	Leu	Gly	Leu	Arg	Arg	Leu	Arg	Gln
															45
Arg	Arg	Arg	Leu	Arg	Arg	Glu	Arg	Val	Arg	Ala	Gln	Pro	Cys	Cys	Arg
															60
Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Ala	His	Ser	Arg
															80
Tyr	His	Thr	Val	His	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys		
															90

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1															15

Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
 20 25 30

Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
 35 40 45

Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His Pro Cys Cys Arg
 50 55 60

Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg
 65 70 75 80

Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys
 85 90

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Xaa Xaa Leu Gly Leu Gly Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE OR GLUTAMIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 14
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu	Xaa	Xaa	Xaa	Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Ala
1								5			10			15

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "THREONINE OR VALINE OR
 ISOLEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site

- (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Cys	Cys	Arg	Pro	Xaa	Ala	Xaa	Xaa	Asp	Xaa	Xaa	Ser	Phe	Leu	Asp
1				5					10			15		

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Ala
1				5				10		

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7

(D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 9

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe Arg Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /note= "ISOLEUCINE OR THREONINE OR VALINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 7

(D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 8

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Cys Cys Arg Pro Xaa Ala Xaa Xaa Asp Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ala Xaa Xaa Asp Xaa Xaa Ser Phe Leu Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys
1 5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 4
 - (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 11
 - (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 13
 - (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu	Xaa	Xaa	Xaa	Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa
1												

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTNWSNGANY TNGGNYNTNGG NTA

23

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTYMGNTAYT GYDSNGGNDS NTGYGANKCN GC

32

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GONGMNTCRC ANSHNCCNSH RCARTANCR AA

32

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCRTCNTCRW ANGCNRYNGG NCKRCARCA

29

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCTNARRAANS WNAVNTCRTC NTCRWANGC

29

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GARRMNBTNH TNTTYMGNTA YTG

23

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GARRMNBTNH TNTTYMGNTA YTGYDSNGGN DSNTGHGA

38

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGAGGGAGAG CGCGCGGTGG TTTCGTCCGT GTGCCCGCG CCCGGCGCTC CTCGCGTGGC	60
CCCGCGTCCT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTC ACTGAGCCCG	120
GCGAGCCCGG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCCATGG CCCGGCCCGT	180
GTCCCGCACCC CTGTGCGGTG GCCTCCTCCG GCACGGGGTC CCCGGTTCGC CTCCGGTCCC	240
CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGGCG GGCTCGGGTG GTCGGAGGAG	300
TCACCACTGA CCGGGTCATC TGGAGCCCGT GGCAGGCCGA GGCCCAGGAT GAGGCGCTGG	360
AAGGCAGCGG CCCTGGTGTG GCTCATCTGC AGCTCCCTGC TATCTGTCTG GATGTGCCAG	420
GAGGGTCTGC TCTTGGGCCA CCGCCTGGGA CCCGCGCTTG CCCCCCTACG ACGCCCTCCA	480
CGCACCCCTGG ACGCCCGCAT CGCCCGCCTG GCCCAGTATC GCGCTCTGCT CCAGGGCGCC	540
CCCGACGCGG TGGAGCTTCG AGAACTTTCT CCCTGGGCTG CCCGCATCCC GGGACCGCGC	600
CGTCGAGCGG GTCCCCGGCG TCGCGGGCG CGGGCGGGGG CTCGGCCTTG TGGGCTGCGC	660
GAGCTCGAGG TGCGCGTGAG CGAGCTGGGC CTGGGCTACA CGTCCGGATGA GACCGTGCTG	720
TTCCGCTACT GCGCAGGCGC GTGCGAGGCG GGCATCCGCA TCTACGACCT GGGCCTTCGG	780

CGCCTGCCGC	AGCGGAGGCG	CGTGCAGA	GAGCGGGCGC	GGGCGCACCC	GTGTTGTCGC	840
CCGACGGCCT	ATGAGGACGA	GGTGTCTTC	CTGGACGTGC	ACAGCCGCTA	CCACACGCTG	900
CAAGAGCTGT	CGGCGGGGA	GTGCGCGTGC	GTGTGATGCT	ACCTCACGCC	CCCCGACCTG	960
CGAAAGGGCC	CTCCCTGCCG	ACCCTCGCTG	AGAACTGACT	TCACATAAAG	TGTGGAACT	1020
CCC						1023

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CCNACNGCNT AYGARGA

17

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1					5					10				15	

Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
					20			25					30		

Asp	Ala	Ala	Glu	Thr	Thr	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
					35			40				45			

Asn	Arg	Arg	Leu	Val	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
					50			55			60				

Ile	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
					65			70			75		80		

His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
					85						90				

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ARYTCYTGNA RNGTRTGRTA

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GACCGAGGTGT CCTTCCTGGA CGTACACA

28

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TAGCGGCTGT GTACGTCCAG GAAGGCACCC TCGT

34

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGCGACGAC GCGTGCACAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TAYGARGACG AGGTGTCCTT CCTGGACGTA CACAGCCGCT AYCAYAC

47

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCGGCCATCC GCATCTACGA CCTGGG

26

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CRTAGGCCGT CGGGCGRCAR CACGGGT

27

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCGCCGAAGG CCCAGGTCGT AGATGCG

27

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGCTACTGCG CAGGCGCGTG CGARGCGGC

29

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGCCGACAGC TCTTGCAGCG TRTGGTA

27

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAGCTGGGCC TGGGCTACGC GTGGGACGAG

30

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCGACGCGTA CCATGAGGCG CTGGAAGGCA GCGGCCCTG

39

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GACCATATGC CGGGGGCTCG GCCTTGTGG

29

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CAGCGACGAC GCGTGCGCAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TAGCGGCTGT GTACGTCCAG GAAGGCACCC TCGT

34

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAAAAATCGGG GGTGYGTCTT A

21

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CATGCCTGGC CTACYTTGTC A

21

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTGGCGTCCC AMCAAGGGTC TTCG

24

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCCAGTGGTG CCGTCGAGGC GGG

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GGCCCAGGAT GAGGCCCTGG AAGG

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCACTCCACT GCCTGAWATT CWACCCC

27

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCATGTGATT ATCGACCATT CGGC

24

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser	Pro	Asp	Lys	Gln	Met	Ala	Val	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg
1					5			10					15		

Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30

Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45

Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60

Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
 65 70 75 80

Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
 85 90 95

Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
 100 105 110

Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125

Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
 1 5 10 15

Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30

Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45

Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60

Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ser Ala Glu Thr Met Tyr Asp
 65 70 75 80

Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys
 85 90 95

Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser
 100 105 110

Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125

Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser	Pro	Asp	Lys	Gln	Ala	Ala	Ala	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg
1				5					10					15	

Gln	Ala	Ala	Ala	Ala	Ser	Pro	Glu	Asn	Ser	Arg	Gly	Lys	Gly	Arg	Arg
				20				25				30			

Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His	Leu
	35				40						45				

Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile
	50				55				60						

Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys	Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp
65				70				75				80			

Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg	Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys
		85					90				95				

Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro	Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser
	100					105				110					

Phe	Leu	Asp	Asp	Ser	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	Ala
115					120					125					

Lys	Arg	Cys	Gly	Cys	Ile										
	130														

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala	Glu	Leu	Gly
1				5				10				15	

Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys
		20			25					30					

Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg
	35					40					45				

Gly	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser	Tyr
	50				55				60						

Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu Pro
65 70 75 80

Gln Leu Ser Ala Ala Ala Cys Gly Cys
85

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
1 5 10 15

Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
20 25 30

Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val
35 40 45

Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys
50 55 60

Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His
65 70 75 80

Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Cys Gly Cys Gly Gly
85 90 95

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

This sequence is intentionally skipped.

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15

Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30

Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45

Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60

Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
 65 70 75 80

Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15

Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30

Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45

Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60

Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
 65 70 75 80

Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly
 85 90

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TGCCGACTGT	GGAGCCTGAC CCTACCAGTG GCTGAGCTGG GCCTGGGCTA TGCCTCGGAG	60
GAGAAGGTCA	TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGCCG TACCCAGCAC	120
AGTCTGGTAC	TGGCCCGGCT TCGAGGGCGG GGTCGAGCCC ATGGCCGACC CTGCTGCCAG	180
CCCACCAGCT	ATGCTGATGT GACCTTCCTT GATGATCAGC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG	CTGCAGCTTG TGGCTGT	267

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TGCCGGCTGT	GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	60
GAGAAGATTA	TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	120
AGTCTGGTGC	TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	180
CCCACCAGCT	ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG	CCGCAGCTTG TGGCTGT	267

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCCGGCTGT	GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	60
GAGAAGATTA	TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	120
AGTCTGGTGC	TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	180
CCCACCAGCT	ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG	CCGCAGCTTG TGGCTGTGGT GGC	273

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1														15	
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
			20						25					30	
Glu	Ser	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
			35					40						45	
Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
			50				55							60	
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
			65			70			75					80	
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys	Ile		
			85					90							

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1														15	
Tyr	Thr	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg	Tyr	Cys	Ala	Gly	Ala	Cys
			20					25						30	
Glu	Ala	Ala	Ile	Arg	Ile	Tyr	Asp	Leu	Gly	Leu	Arg	Arg	Leu	Arg	Gln
			35					40						45	
Arg	Arg	Arg	Val	Arg	Arg	Glu	Arg	Ala	Arg	Ala	His	Pro	Cys	Cys	Arg
			50				55							60	
Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Val	His	Ser	Arg
			65			70			75					80	
Tyr	His	Thr	Leu	Gln	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys	Val	
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala	Glu	Leu	Gly	Leu	Gly
1				5				10						15	
Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys
			20				25						30		
Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg
	35					40							45		
Gly	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser	Tyr
	50				55						60				
Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	Gln	His	His	Trp	Gln	Gln	Leu	Pro
	65				70				75					80	
Gln	Leu	Ser	Ala	Ala	Cys	Gly	Cys	Gly	Gly						
					85				90						

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGCCTCAGAG GAGAAGATTA TC

22

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Ala Ser Glu Glu Lys Ile Ile
1 5

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGTCGGGGTT GGGGTATGCC TCA

23

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TATGCCTCAG AGGAGAAAGAT TATCTT

26

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCTCAGAGGA GAAGATTATC TTCCGATACT GTGCTGGCAG CTGTCCCCAA GAGGTCCGTA	60
CCCAGCACAG TCTGGTGCTG GCCCGTCTTC GAGGGCAGGG TCGAGCTCAT GGCAGACCTT	120
GCTGCCAGCC CACCAGCTAT GCTGATGTGA CCTTCCTTGA TGACCACACC CATTGGCAGC	180
AGCTGCCTCA GCTCTCAGCC GCAGCTTGTG GCTGTGGTGG CTGAAGGCAG CCAGCCTGGT	240
CTCTCAGAAT CACAAGCAAG AGGCAGCCTT TGAAAGGCTC AGGTGACGTT ATTAGAAACT	300
TGCATAGGAG AAGATTAAGA AGAGAAAGGG GACCTG	336

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Lys Asp
1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCATCAAGGA AGGTCACATC AGCATA

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCACCAACAGC CACAAGCTGC GGSTGAGAGC TG

32

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Ala Leu Ala Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GAGGGACCTG	GACGCCCAT	CAGGGTAAGA	ATTCCCTGGGG	GCCTCCCGAC	TCCCCAATTC	60
CTTCTCTCAA	AGCCCTCACT	TTGCCTTACA	ATCCTACTCT	ACCTTGCACT	AGGTAACAAAC	120
CATGTCCGTC	TTCCAAGAGC	CTTGGCTGGT	TCATGCCGAC	TGTGGAGCCT	GACCCTACCA	180
GTGGCTGAGC	TGGGCCTGGG	CTATGCCTCG	GAGGAGAAGG	TCATCTTCCG	ATACTGTGCT	240
GGCAGCTGTC	CCCAAGAGGC	CCGTACCCAG	CACAGTCTGG	TACTGGCCCG	GCTTCGAGGG	300
CGGGGTCGAG	CCCATGCCG	ACCCGTCTGC	CAGCCCACCA	GCTATGCTGA	TGTGACCTTC	360
CTTGATGATC	AGCACCATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCTGCAGC	TTGTGGCTGT	420
GGTGGCTGAA	GGAGGCCAGT	CTGGTGTCTC	AGAACACAA	GCATGAGACA	GGCTGGGCTT	480
TGAAAGGCTC	AGGTGACATT	ACTAGAAATT	TGCATAGGTA	AAGATAAGAA	GGGAAAGGAC	540
CAGG						544

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Ser	Glu	Glu	Lys	Ile	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys	Pro	Gln
1						5				10					15
Glu	Val	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg	Gly	Gln
	20						25				30				
Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser	Tyr	Ala	Asp
	35					40					45				
Val	Thr	Phe	Leu	Asp	Asp	His	His	His	Trp	Gln	Gln	Leu	Pro	Gln	Leu
	50					55					60				
Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly							
	65				70										

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TGCCGGCTGT	GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	60
GAGAAAGATTA	TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	120
AGTCTGGTGC	TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	180
CCCACCAGCT	ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG	CGGCAGCTTG TGGCTGTGGT GGCTGAAGGC GGCCAGCCTG GTCTCTCAGA	300
ATCACAAAGCA	AGAGGCAGCC TTTGAAAGGC TCAGGTGACG TTATTAGAAA CTTGCATAGG	360
AGAAGATTA	GAAGAGAAAG GGGACCTGAT T	391

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "SERINE, THREONINE, OR

ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Val Xaa Xaa Leu Gly Leu Gly Tyr	
1	5

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID, GLUTAMIC ACID OR NO AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "valine or aspartic acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Asp Xaa Xaa Xaa Phe Leu Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Glu Gly Pro Gly Arg Pro Ile Arg Val Arg Ile Pro Gly Gly Leu Pro
1 5 10 15

Thr Pro Gln Phe Leu Leu Ser Lys Pro Ser Leu Cys Leu Thr Ile Leu
20 25 30

Leu Tyr Leu Ala Leu Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu
35 40 45

Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu
 50 55 60

Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala
 65 70 75 80

Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala
 85 90 95

Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro
 100 105 110

Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln
 115 120 125

Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 130 135 140

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ala Leu Pro Gly Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, GLUTAMIC ACID OR LYSINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE, LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "ARGININE OR GLUTAMINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "THREONINE, VALINE OR
 ISOLEUCINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC
 ACID OR ALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC
 ACID OR NO AMINO ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 12
 (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Cys	Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Phe	Leu	Asp	Xaa
1				5					10				15		

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTNDGNGANY TGGGNYTGGG NTA

23

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GANBTNWCNT TYYTNGANG

19

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GANBTNWCNT TYYTNGANGW

20

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTYMGNTAYT GYDSNGGNDS NTG

23

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GTNDGNGANY TGGGNYTNGG

20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GTNDGNGANY TGGGNYTGGG NTT

23

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

WCNTCNARRA ANGWNNAVNTC

20

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

WCNTCNARRA ANGWNNAVNT

19

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CANSHNCCNS HRCARTANCK RAA

23

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CANSHNCCNS HRCARTANCK RAANA

25

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Val Xaa Xaa Leu Gly Leu Gly Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "THREONINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Xaa Phe Leu Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 7

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 3

(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Val Xaa Xaa Leu Gly Leu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Val	Xaa	Xaa	Leu	Gly	Leu	Gly	Phe
1							5

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Xaa	Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys
1							5	

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCCTTGCA CCCGAGCCTC	60
GGCTGGGTCC TTGATCTTCA AGAGGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG	120
GCAGAGACTA GAGGGACCTG GACGCCCAT CAGGGTAAGA ATTCCCTGGGG GCCTCCCGAC	180

TCCCCAATTC	CTTCTCTCAA	AGCCCTCACT	TTGCCTTACA	ATCCTACTCT	ACCTTGCACT	240
AGGTAACAAAC	CATGTCCGTC	TTCCAAGAGC	CTTGGCTGGT	TCATGCCGAC	TGTGGAGCCT	300
GACCCTACCA	GTGGCTGAGC	TGGGCCTGGG	CTATGCCCTCG	GAGGAGAAGG	TCATCTTCCG	360
ATACTGTGCT	GGCAGCTGTC	CCCAAGAGGC	CCGTACCCAG	CACAGTCTGG	TACTGGCCCG	420
GCTTCGAGGG	CGGGGTCGAG	CCCATGGCCG	ACCCTGCTGC	CAGCCCACCA	GCTATGCTGA	480
TGTGACCTTC	CTTGATGATC	AGCACCAATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCTGCAGC	540
TTGTGGCTGT	GGTGGCTGA					559

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Pro	Asp	Ala	Arg	Gly	Val	Pro	Val	Ala	Asp	Gly	Glu	Phe	Ser	Ser	Glu
1					5						10				15
Gln	Val	Ala	Lys	Ala	Gly	Gly	Thr	Trp	Leu	Gly	Thr	His	Arg	Pro	Leu
							20		25					30	
Ala	Arg	Leu	Arg	Arg	Ala	Leu	Ser	Gly	Pro	Cys	Gln	Leu	Trp	Ser	Leu
							35		40					45	
Thr	Leu	Ser	Val	Ala	Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys
							50		55					60	
Val	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys	Pro	Arg	Gly	Ala	Arg	Thr
							65		70					75	80
Gln	His	Gly	Leu	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Gln	Gly	Arg	Ala	His
							85		90					95	
Gly	Gly	Pro	Cys	Cys	Arg	Pro	Thr	Arg	Tyr	Thr	Asp	Val	Ala	Phe	Leu
							100		105					110	
Asp	Asp	Arg	His	Arg	Trp	Gln	Arg	Leu	Pro	Gln	Leu	Ser	Ala	Ala	
							115		120					125	
Cys	Gly	Cys	Gly	Gly											
							130								

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
1 5 10 15

Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
20 25 30

Glu Ala Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
35 40 45

Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
50 55 60

Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr
65 70 75 80

His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
85 90

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Ser Leu
1 5 10 15

His Pro Ser Leu Gly Trp Val
20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met	Ala	Ala	Gly	Arg	Leu	Arg	Ile	Leu	Phe	Leu	Leu	Leu	Ser	Leu
1				5					10				15	
His Leu Gly Leu Gly Trp Val														
20														

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

AATCCCCAGG ACAGGCAGGG AAT 23

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGGTACCCAG ATCTTCAGCC ACCACAGCCA CAAGC 35

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGACTATCAT ATGGCCCACC ACCACCACCA CCACCACAC GACCGACGACG ACAAGGCCTT 60

GGCTGGTTCA TGCCGA

76

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TGCTGTCACC ATGGCTGCAG GAAGACTTCG GA

32

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Ala	Leu	Ala	Gly	Ser	Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala
1															15

Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr
20															30

Cys	Ala	Gly	Ser	Cys	Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val
35															45

Leu	Ala	Arg	Leu	Arg	Gly	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys
50															60

Arg	Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Val	His	Ser
65															80

Arg	Tyr	His	Thr	Leu	Gln	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys	Val
85															95

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TAATACGACT CACTATAGGG GAA

23

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TCGTCTTCGT AAGCAGTCGG ACGGCAGCAG GGTCGGCCAT GGGCTCGAC

49

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGCTGCCGTC CGACTGCTTA CGAAGACGA

29

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GTTATGCTAG TTATTGCTCA GCGGT

25

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Val Ser
 1 5 10 15

Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 20 25 30

Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
 35 40 45

Arg Arg Leu Arg Gln Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
 50 55 60

His Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp
 65 70 75 80

Asp Gln His His Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys
 85 90 95

Gly Cys Gly Gly
 100

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CACATCAGCA TAGCTGGTGG GCTGGCAGCA CGGGTGAGCA CGAGCACGTT

50

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TGCTGCCAGC CCACCAGCTA TGCTG

25

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CCTCGGAGGA GAAGGTATC TTC

23

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Cys Cys Val Arg Gln Ile Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp
1 5 10 15

Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly
20 25 30

Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu
35 40 45

Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys
50 55 60

Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg
65 70 75 80

Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys
85 90 95

Cys Ser

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp
1 5 10 15

Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly
 20 25 30

Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu
 35 40 45

Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
 50 55 60

Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys
 65 70 75 80

Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys
 85 90 95

Cys Ser

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp
 1 5 10 15

Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly
 20 25 30

Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu
 35 40 45

Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
 50 55 60

Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg
 65 70 75 80

Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys
 85 90 95

Cys Ser

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Cys	Cys	Lys	Lys	Gln	Phe	Phe	Val	Ser	Phe	Lys	Asp	Ile	Gly	Trp	Asn
1				5					10					15	
Asp	Trp	Ile	Ile	Ala	Pro	Ser	Gly	Tyr	His	Ala	Asn	Tyr	Cys	Glu	Gly
	20						25						30		
Glu	Cys	Pro	Ser	His	Ile	Ala	Gly	Thr	Ser	Gly	Ser	Ser	Leu	Ser	Phe
	35					40					45				
His	Ser	Thr	Val	Ile	Asn	His	Tyr	Arg	Met	Arg	Gly	His	Ser	Pro	Phe
	50					55				60					
Ala	Asn	Leu	Lys	Ser	Cys	Cys	Val	Pro	Thr	Lys	Leu	Arg	Pro	Met	Ser
	65				70				75				80		
Met	Leu	Tyr	Tyr	Asp	Asp	Gly	Gln	Asn	Ile	Ile	Lys	Lys	Asp	Ile	Gln
				85					90				95		
Asn	Met	Ile	Val	Glu	Glu	Cys	Gly	Cys	Ser						
			100						105						

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Cys	Cys	Arg	Gln	Gln	Phe	Phe	Ile	Asp	Phe	Arg	Leu	Ile	Gly	Trp	Asn
1				5					10				15		
Asp	Trp	Ile	Ile	Ala	Pro	Thr	Gly	Tyr	Tyr	Gly	Asn	Tyr	Cys	Glu	Gly
	20					25					30				
Ser	Cys	Pro	Ala	Tyr	Leu	Ala	Gly	Val	Pro	Gly	Ser	Ala	Ser	Ser	Phe
	35					40					45				
His	Thr	Ala	Val	Val	Asn	Gln	Tyr	Arg	Met	Arg	Gly	Leu	Asn	Pro	Gly
	50				55					60					
Thr	Val	Asn	Ser	Cys	Cys	Ile	Pro	Thr	Lys	Leu	Ser	Thr	Met	Ser	Met
	65					70			75				80		
Leu	Tyr	Phe	Asp	Asp	Glu	Tyr	Asn	Ile	Val	Lys	Arg	Asp	Val	Pro	Asn
				85					90				95		
Met	Ile	Val	Glu	Glu	Cys	Gly	Cys	Ala							
			100					105							

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Cys	Arg	Arg	Val	Lys	Phe	Gln	Val	Asp	Phe	Asn	Leu	Ile	Gly	Trp	Gly
1				5				10						15	
Ser	Trp	Ile	Ile	Tyr	Pro	Lys	Gln	Tyr	Asn	Ala	Tyr	Arg	Cys	Glu	Gly
	20						25						30		
Glu	Cys	Pro	Asn	Pro	Val	Gly	Glu	Glu	Phe	His	Pro	Thr	Asn	His	Ala
	35				40				45						
Tyr	Ile	Gln	Ser	Leu	Leu	Lys	Arg	Tyr	Gln	Pro	His	Arg	Val	Pro	Ser
	50					55			60						
Thr	Cys	Cys	Ala	Pro	Val	Lys	Thr	Lys	Pro	Leu	Ser	Met	Leu	Tyr	Val
	65				70				75					80	
Asp	Asn	Gly	Arg	Val	Leu	Leu	Glu	His	His	Lys	Asp	Met	Ile	Val	Glu
				85				90					95		
Glu	Cys	Gly	Cys	Leu											
				100											

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Cys	Lys	Arg	His	Pro	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn
1					5			10						15	
Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	His	Ala	Phe	Tyr	Cys	His	Gly
		20					25						30		
Glu	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala
		35				40						45			
Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Lys	Ile	Pro	Lys	Ala
		50				55					60				
Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp
		65			70				75					80	
Glu	Asn	Glu	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Asp	Met	Val	Val	Glu
				85				90					95		
Gly	Cys	Gly	Cys	Arg											
				100											

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn
1				5					10				15		
Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala	Phe	Tyr	Cys	His	Gly
		20						25					30		
Asp	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala
		35						40				45			
Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser	Ile	Pro	Lys	Ala
		50				55					60				
Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp
		65			70				75			80			
Glu	Tyr	Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met	Val	Val	Glu
		85						90				95			
Gly	Cys	Gly	Cys	Arg											
				100											

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asp
1				5					10				15		
Asp	Trp	Ile	Val	Ala	Pro	Leu	Gly	Tyr	Asp	Ala	Tyr	Tyr	Cys	His	Gly
		20						25					30		
Lys	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Phe	Asn	Ser	Thr	Asn	His	Ala
		35						40				45			
Val	Val	Gln	Thr	Leu	Val	Asn	Asn	Met	Asn	Pro	Gly	Lys	Val	Pro	Lys
		50				55					60				
Ala	Cys	Cys	Val	Pro	Thr	Gln	Leu	Asp	Ser	Val	Ala	Met	Leu	Tyr	Leu
		65			70				75			80			

Asn Asp Gln Ser Thr Val Val Leu Lys Asn Tyr Gln Glu Met Thr Val
 85 90 95

Val Gly Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 1 5 10 15

Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
 20 25 30

Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45

Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
 50 55 60

Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80

Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95

Arg Ser Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
 1 5 10 15

Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
 20 25 30

Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45

Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly
 20 25 30
 Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu
 1 5 10 15

Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly
 20 25 30
 Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys
 50 55 60
 Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr
 65 70 75 80
 Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val
 85 90 95
 Lys Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp His
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser Gly
 20 25 30
 Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr His
 65 70 75 80
 Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile Val
 85 90 95
 Lys Ser Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
 1 5 10 15

Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser Gly
 20 25 30

Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
 35 40 45

Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile Pro
 50 55 60

Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu Phe
 65 70 75 80

Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met Thr
 85 90 95

Val Glu Ser Cys Ala Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys Asp Val Gly Trp Gln
 1 5 10 15

Asn Trp Val Ile Ala Pro Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly
 20 25 30

Glu Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly Ser Asn His Ala
 35 40 45

Ile Leu Gln Thr Leu Val His Ser Ile Glu Pro Glu Asp Ile Pro Leu
 50 55 60

Pro Cys Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met Leu Phe Tyr
 65 70 75 80

Asp Asn Asn Asp Asn Val Val Leu Arg His Tyr Glu Asn Met Ala Val
 85 90 95

Asp Glu Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Cys	Arg	Ala	Arg	Arg	Leu	Tyr	Val	Ser	Phe	Arg	Glu	Val	Gly	Trp	His
1					5				10					15	
Arg	Trp	Val	Ile	Ala	Pro	Arg	Gly	Phe	Leu	Ala	Asn	Tyr	Cys	Gln	Gly
			20						25				30		
Gln	Cys	Ala	Leu	Pro	Val	Ala	Leu	Ser	Gly	Ser	Gly	Gly	Pro	Pro	Ala
			35				40					45			
Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His	Ala	Ala	Ala	Pro	Gly
			50			55				60					
Ala	Ala	Asp	Leu	Pro	Cys	Cys	Val	Pro	Ala	Arg	Leu	Ser	Pro	Ile	Ser
			65		70				75				80		
Val	Leu	Phe	Phe	Asp	Asn	Ser	Asp	Asn	Val	Val	Leu	Arg	Gln	Tyr	Glu
			85				90					95			
Asp	Met	Val	Val	Asp	Glu	Cys	Gly	Cys	Arg						
			100					105							

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Cys	His	Arg	His	Gln	Leu	Phe	Ile	Asn	Phe	Gln	Asp	Leu	Gly	Trp	His
1					5				10					15	
Lys	Trp	Val	Ile	Ala	Pro	Lys	Gly	Phe	Met	Ala	Asn	Tyr	Cys	His	Gly
			20				25					30			
Glu	Cys	Pro	Phe	Ser	Met	Thr	Thr	Tyr	Leu	Asn	Ser	Ser	Asn	Tyr	Ala
			35			40					45				
Phe	Met	Gln	Ala	Leu	Met	His	Met	Ala	Asp	Pro	Lys	Val	Pro	Lys	Ala
			50			55				60					
Val	Cys	Val	Pro	Thr	Lys	Leu	Ser	Pro	Ile	Ser	Met	Leu	Tyr	Gln	Asp
			65			70			75				80		
Ser	Asp	Lys	Asn	Val	Ile	Leu	Arg	His	Tyr	Glu	Asp	Met	Val	Val	Asp
			85				90				95				
Glu	Cys	Gly	Cys	Gly											
			100												

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Cys	Arg	Arg	Thr	Ser	Leu	His	Val	Asn	Phe	Lys	Glu	Ile	Gly	Trp	Asp
1															
															15
Ser	Trp	Ile	Ile	Ala	Pro	Lys	Asp	Tyr	Glu	Ala	Phe	Glu	Cys	Lys	Gly
															30
Gly	Cys	Phe	Phe	Pro	Leu	Thr	Asp	Asn	Val	Thr	Pro	Thr	Lys	His	Ala
															45
Ile	Val	Gln	Thr	Leu	Val	His	Leu	Gln	Asn	Pro	Lys	Lys	Ala	Ser	Lys
															50
															55
Ala	Cys	Cys	Val	Pro	Thr	Lys	Leu	Asp	Ala	Ile	Ser	Ile	Leu	Tyr	Lys
															60
Asp	Asp	Asp	Ala	Gly	Val	Pro	Thr	Leu	Ile	Tyr	Asn	Tyr	Glu	Gly	Met
															95
Val	Ala	Glu	Cys	Gly	Gly	Cys	Arg								
															100

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Cys	His	Arg	Val	Ala	Leu	Asn	Ile	Ser	Phe	Gln	Glu	Leu	Gly	Trp	Glu
1															
															15
Arg	Trp	Ile	Val	Tyr	Pro	Pro	Ser	Phe	Ile	Phe	His	Tyr	Cys	His	Gly
															30
Gly	Cys	Gly	Leu	His	Ile	Pro	Pro	Asn	Leu	Ser	Leu	Pro	Val	Pro	Gly
															45
Ala	Pro	Pro	Thr	Pro	Ala	Gln	Pro	Tyr	Ser	Leu	Leu	Pro	Gly	Ala	Gln
															50
															55
Pro	Cys	Cys	Ala	Ala	Leu	Pro	Gly	Thr	Met	Arg	Pro	Leu	His	Val	Arg
															60
65															70
75															

Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro Asn
 85 90 95

Leu Leu Thr Gln His Cys Ala Cys Ile
 100 105

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser Val
 1 5 10 15

Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Ala Cys Gly
 20 25 30

Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val Leu
 35 40 45

Leu Leu Lys Met Gln Ala Arg Gly Ala Thr Leu Ala Arg Pro Pro Cys
 50 55 60

Cys Val Pro Thr Ala Tyr Thr Gly Lys Leu Leu Ile Ser Leu Ser Glu
 65 70 75 80

Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu Cys
 85 90 95

Gly Cys Arg

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Cys Glu Leu His Asp Phe Ser Leu Ser Phe Ser Gln Leu Lys Trp Asp
 1 5 10 15

Asn Trp Ile Val Ala Pro His Ser Tyr Asn Pro Ser Tyr Cys Lys Gly
 20 25 30

Asp Cys Pro Ser Ala Val Ser His Arg Tyr Gly Ser Pro Val His Thr
 35 40 45

Met Val Gln Asn Met Ile Tyr Glu Lys Leu Asp Pro Ser Val Pro Ser
 50 55 60
 Pro Ser Cys Val Pro Gly Lys Tyr Ser Pro Leu Ser Val Leu Thr Ile
 65 70 75 80
 Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Met Ala
 85 90 95
 Thr Ser Cys Thr Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 1 5 10 15
 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
 20 25 30
 Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
 35 40 45
 Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
 50 55 60
 Ile Ala Phe Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
 65 70 75 80
 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
 85 90

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
 20 25 30

Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
 35 40 45

Arg Arg Arg Leu Arg Arg Glu Arg Val Arg Ala Gln Pro Cys Cys Arg
 50 55 60

Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His Ser Arg
 65 70 75 80

Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys Val
 85 90 95

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Leu Asp Leu Gln Glu Ala Ser Val Ala Asp Lys Leu Ser Phe Gly Lys
 1 5 10 15

Met Ala Glu Thr Arg Gly Thr Trp Thr Pro His Gln Gly Asn Asn His
 20 25 30

Val Arg Leu Pro Arg
 35

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Leu Asp Leu Gln Glu Ala Pro Ala Ala Asp Glu Leu Ser Ser Gly Lys
 1 5 10 15

Met Ala Glu Thr Gly Arg Thr Trp Lys Pro His Gln Gly Asn Asn Asn
 20 25 30

Val Arg Leu Pro Arg
 35

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1					5					10				15	

Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
							20		25				30		

Glu	Ser	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
					35			40				45			

Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
					50			55			60				

Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
					65			70			75		80		

His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
				85				90							

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ATGGCTGCAG	GAAGACTTCG	GATCCTGTGT	CTGCTGCTCC	TGTCCTTGCA	CCCGAGCCTC	60
GGCTGGTCC	TTGATCTTCA	AGAGGCTTCT	GTGGCAGATA	AGCTCTCATT	TGGGAAGATG	120
GCAGAGACTA	GAGGGACCTG	GACGCCCAT	CAGGGTAAGA	ATT CCTGGGG	GCCTCCCGAC	180
TCCCCAATTC	CTTCTCTCAA	AGCCCTCACT	TTGCCCTACA	ATCCTACTCT	ACCTTGCACT	240
AGGTAACAAAC	CATGTCCGTC	TTCCAAGAGC	CTTGGCTGGT	TCATGCCGAC	TGTGGAGCCT	300
GACCCTACCA	GTGGCTGAGC	TGGGCTGGG	CTATGCCCTCG	GAGGAGAAGG	TCATCTTCCG	360
ATACTGTGCT	GGCAGCTGTC	CCCAAGAGGC	CCGTACCCAG	CACAGTCTGG	TACTGGCCCG	420
GCTTCGAGGG	CGGGGTCGAG	CCCATGGCCG	ACCCCTGCTG	CAGCCCACCA	GCTATGCTGA	480
TGTGACCTTC	CTTGATGATC	AGCACCAATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCTGCAGC	540
TTGTGGCTGT	GGTGGCTGAA	GGAGGCCAGT	CTGGTGTCTC	AGAACATCACAA	GCATGAGACA	600
GGCTGGGCTT	TGAAAGGCTC	AGGTGACATT	ACTAGAAATT	TGCATAGGTA	AAGATAAGAA	660
GGGAAAGGAC	CAGGGGTTTT	TTGTTTCTTT	CTTGCTTGC	TTGTTAGTTT	TTTTTTTTTT	720

TTT 723

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 723 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AAAAAAA	AA	AAACTAA	CAAGCAAGCA	AAGAAAGAAA	CAAAAAACCC	CTGGTCCTTT	60
CCCTTCTTAT	CTTTACCTAT	GCAAATTCT	AGTAATGTCA	CCTGAGCCTT	TCAAAGCCCC		120
GCCTGTCTCA	TGCTTGAT	TCTGAGACAC	CAGACTGGCC	TCCTTCAGCC	ACCACAGCCA		180
CAAGCTGCAG	CTGAGAGCTG	AGGCAGCTGC	TGCCAATGGT	GCTGATCATC	AAGGAAGGTC		240
ACATCAGCAT	AGCTGGTGGG	CTGGCAGCAG	GGTCGGCCAT	GGGCTCGACC	CCGCCCTCGA		300
AGCCGGGCCA	GTACCAAGACT	GTGCTGGTA	CGGGCCTCTT	GGGGACAGCT	GCCAGCACAG		360
TATCGGAAGA	TGACCTTCTC	CTCCGAGGCA	TAGCCCAGGC	CCAGCTCAGC	CACTGGTAGG		420
GTCAGGCTCC	ACAGTCGGCA	TGAACCAGCC	AAGGCTCTTG	GAAGACGGAC	ATGGTTGTTA		480
CCTAGTGCAA	GGTAGAGTAG	GATTGTAAGG	CAAAGTGAGG	GCTTGAGAG	AAGGAATTGG		540
GGAGTCGGGA	GGCCCCCAGG	AATTCTTACC	CTGATGGGC	GTCCAGGTCC	CTCTAGTCTC		600
TGCCATCTTC	CCAAATGAGA	GCTTATOTGC	CACAGAACCC	TCTTGAAGAT	CAAGGACCCA		660
GCCGAGGCTC	GGGTGCAAGG	ACAGGACAG	CAGACACAGG	ATCCGAAGTC	TTCCTGCAGC		720
CAT							723

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ATGGCTGCAG	GAAGACTTCG	GATCCTGTGT	CTGCTGCTCC	TGTCCTTGCA	CCCGAGCCTC	60
GGCTGGGTCC	TTGATCTTCA	AGAGGCTTCT	GTGGCAGATA	AGCTCTCATT	TGGGAAGATG	120
GCAGAGACTA	GAGGGACCTG	GACGCCCAT	CAGGGTAACA	ACCATGTCCG	TCTTCCAAGA	180
GCCTTGGCTG	GTTCATGCCG	ACTGTGGAGC	CTGACCCTAC	CAGTGGCTGA	GCTGGGCCTG	240

GGCTATGCCT	CGGAGGAGAA	GGTCATCTTC	CGATACTGTG	CTGGCAGCTG	TCCCCAAGAG	300
GCCCGTACCC	AGCACAGTCT	GGTACTGGCC	CGGCTTCGAG	GGCGGGGTCG	AGCCCATGGC	360
CGACCCCTGCT	CCCAGCCCAC	CAGCTATGCT	GATGTGACCT	TCCTTGATGA	TCAGCACCAT	420
TGGCAGCAGC	TGCCTCAGCT	CTCAGCTGCA	GCTTGTGGCT	GTGGTGGCTG	A	471

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

TCAGGCCACCA	CAGCCACAAG	CTGCAGCTGA	GAGCTGAGGC	AGCTGCTGCC	AATGGTGCTG	60
ATCATCAAGG	AAGGTACACAT	CAGCATAGCT	GGTGGGCTGG	CAGCAGGGTC	GGCCATGGC	120
TCGACCCCCG	CCTCGAACGCC	GGGCCAGTAC	CAGACTGTGC	TGGGTACGGG	CCTCTTGGGG	180
ACAGCTGCCA	GCACAGTATC	GGAAAGATGAC	CTTCTCCTCC	GAGGCATAGC	CCAGGCCCAG	240
CTCAGCCACT	GGTAGGGTCA	GGCTCCACAG	TCGGCATGAA	CCAGCCAAGG	CTCTTGGAAAG	300
ACGGACATGG	TTGTTACCCCT	GATGGGGCGT	CCAGGTCCCT	CTAGTCTCTG	CCATCTTCCC	360
AAATGAGAGC	TTATCTGCCA	CAGAAGCCTG	TTGAAGATCA	AGGACCCAGC	CGAGGCTCGG	420
GTGCAAGGAC	AGGAGCAGCA	GACACAGGAT	CCGAAGTCTT	CCTGCAGCCA	T	471

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

ATGGCTGCAG	GAAGACTTCG	GATCCTGTGT	CTGCTGCTCC	TGTCCTTGCA	CCCGAGCCTC	60
GGCTGGGTCC	TTGATCTTCA	AGAGGCTTCT	GTGGCAGATA	AGCTCTCATT	TGGGAAGATG	120
GCAGAGACTA	GAGGGACCTG	GACGCCCAT	CAGGGTAACA	ACCATGTCCG	TCTTCCAAGA	180

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TCTTGGAAAGA CGGACATGGT TGTTACCCCTG ATGGGGCGTC CAGGTCCCTC TAGTCTCTGC	60
CATCTTCCCA AATGAGAGCT TATCTGCCAC AGAACGCCTCT TGAAGATCAA GGACCCAGCC	120
GAGGCTCGGG TGCAAGGACA GGAGCAGCAG ACACAGGATC CGAAGTCTTC CTGCAGCCAT	180

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GCCTTGGCTG GTTCATGCCG ACTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTGGGCCTG	60
GGCTATGCCT CGGAGGAGAA GGTCACTTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG	120
GCCCCGTACCC AGCACAGTCT GGTACTGGCC CGGCTTCGAG GGCGGGGTCG AGCCCATGGC	180
CGACCCCTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA TCAGCACCAT	240
TGGCAGCAGC TGCCTCAGCT CTCAGCTGCA GCTTGTGGCT GTGGTGGCTG A	291

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

TCAGCCACCA CAGCCACAAG CTGCAGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGCTG	60
ATCATCAAGG AAGGTACACAT CAGCATAGCT GGTGGGCTGG CAGCAGGGTC GGCCATGGGC	120
TCGACCCCGC CCTCGAAGCC GGGCCAGTAC CAGACTGTGC TGGGTACGGG CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATGAC CTTCTCCTCC GAGGCATAGC CCAGGCCAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG TCGGCATGAA CCAGCCAAGG C	291

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Ser Leu	1	5	10	15
His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala	20		25	30
Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr	35		40	45
Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu Ala Gly	50		55	60
Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu	65		70	75
Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser	85		90	95
Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu	100		105	110
Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser	115		120	125
Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu	130		135	140
Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly	145		150	155

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Ser Leu	1	5	10	15
His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala	20		25	30

Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr
 35 40 45

Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15

Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 20 25 30

Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val
 35 40 45

Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60

Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His
 65 70 75 80

Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

ATGGCTGCAG GAAGACTTCG GATCTTGTTC CTGCTGCTCC TGTCCCTGCA CCTGGGCCTT	60
GGCTGGGTCC TTGATCTTCA AGAGGCTCCT CGCGCAGATG AGCTCTCATC TGGGAAAATG	120
GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAAGA ATTCTTGGGG GCCTCCTAAC	180
TCTACAGTTC TTCCTCTCAA AGCCCTCACT TTGCCTCACAA ATCCTATTCT ACCTTGCACT	240
AGGTAACAAC AATGTCCGCC TTCCAAGAGC CTTACCTGGT TTGTGCCGGC TGTGGAGCCT	300
GACCCTACCA GTGGCTGAGC TTGGCCTGGG CTATGCCTCA GAGGAGAAGA TTATCTTCCG	360

ATACTGTGCT	GGCAGCTGTC	CCCAAGAGGT	CCGTACCCAG	CACAGTCTGG	TGCTGGCCCG	420
TCTTCGAGGC	CAGGGTCGAG	CTCATGGCAG	ACCTTGCTGC	CAGCCCACCA	GCTATGCTGA	480
TGTGACCTTC	CTTGATGACC	ACCACCATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCCGCAGC	540
TTGTGGCTGT	GGTGGCTGA					559

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 559 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TCAGCCACCA	CAGCCACAAG	CTGCGGCTGA	GAGCTGAGGC	AGCTGCTGCC	AATGGTGGTG	60
GTCATCAAGG	AAGGTACAT	CAGCATAGCT	GGTGGGCTGG	CAGCAAGGTC	TGCCATGAGC	120
TCGACCCTGC	CCTCGAACAC	GGGCCAGCAC	CAGACTGTGC	TGGGTACGGA	CCTCTGGGG	180
ACAGCTGCCA	GCACAGTATC	GGAAAGATAAT	CTTCTCTCT	GAGGCATAGC	CCAGGCCAAG	240
CTCAGCCACT	GGTAGGGTCA	GGCTCCACAG	CCGGCACAAA	CCAGGTAAGG	CTCTTGGAAAG	300
GCGGACATTG	TTGTTACCTA	GTGCAAGGTA	GAATAGGATT	GTGAGGCAGA	GTGAGGGCTT	360
TGAGAGGAAG	AACTGTAGAG	TTAGGAGGCC	CCCAAGAATT	CTTACCCCTGA	TGGGGCTTCC	420
AGGTCTTCC	AGTCTCTGCC	ATTTTCCCAG	ATGAGAGCTC	ATCTGCCGCA	GGAGCCTCTT	480
GAAGATCAAG	GACCCAGCCA	AGGGCCAGGT	GCAAGGACAG	GAGCAGCAGA	AACAAGATCC	540
GAAGTCTTCC	TGCAGCCAT					559

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

ATGGCTGCAG	GAAGACTTCG	GATCTTGTTC	CTGCTGCTCC	TGTCCTTGCA	CCTGGGCCTT	60
GGCTGGGTCC	TTGATCTTCA	AGAGGCTCCT	GGGGCAGATG	AGCTCTCATC	TGGGAAATG	120
GCAGAGACTG	GAAGGACCTG	GAAGCCCCAT	CAGGGTAACA	ACAATGTCCG	CCTTCCAAGA	180
GCCTTACCTG	GTGTTGTGCCG	GCTGTGGAGC	CTGACCCCTAC	CAGTGGCTGA	GCTTGGCCTG	240

GGCTATGCCT	CAGAGGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG	300
GTCCGTACCC	AGCACAGTCT GGTGCTGCC CGTCTCGAG GGCAGGGTCG AGCTCATGGC	360
AGACCTTGCT	GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA CCACCACCAT	420
TGGCAGCAGC	TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A	471

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TCAGCCACCA	CAGCCACAAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG	60
GTCATCAAGG	AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC	120
TCGACCCCTGC	CCTCGAACAG CGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG	180
ACAGCTGCCA	GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG	240
CTCAGCCACT	GGTAGGGTCA GGCTCOACAG CCGGCACAAA CCAGGTAAGG CTCTTGGAAAG	300
GCGGACATTG	TTGTTACCTT GATGGGGCTT CCAGGTCTT CCAGTCTCTG CCATTTTCCC	360
AGATGAGAGC	TCATCTGCCG CAGGPGCCTC TTGAAGATCA AGGACCCAGC CAAGGCCAG	420
GTGCAAGGAC	AGGAGCAGCA GAAAGAAGAT CCGAAGTCTT CCTGCAGCCA T	471

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

ATGGCTGCAG	GAAGACTTCG GATCTTGTCTT CTGCTGCTCC TGTCTTGCA CCTGGGCCTT	60
GGCTGGGTCC	TTGATCTTCA AGAGGCTCT GCAGGAGATG AGCTCTCATC TGGGAAAATG	120
GCAGAGACTG	GAAGGACCTG GAAGCCCCAT CAGGGTAAGA ACAATGTCCG CCTTCCAAGA	180

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TCTTGGAAAGG CGGACATTGT TGTTACCCCTG ATGGGGCTTC CAGGTCCTTC CAGTCTCTGC	60
CATTTTCCCA GATGAGAGCT CATCTGCCGC AGGAGCCTCT TGAAGATCAA GGACCCAGCC	120
AAGGCCAGG TGCAAGGACA GGAGCAGCAG AAACAAGATC CGAAGTCTTC CTGCAGCCAT	180

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GCCTTACCTG GTTTGTGCCG GCTGTGGAGC CTGACCCCTAC CAGTGGCTGA GCTTGGCCTG	60
GGCTATGCCT CAGAGGAGAA GATTATCTTG CGATACTGTG CTGGCAGCTG TCCCCAAGAG	120
GTCCGTACCC AGCACAGTCT GGTGCTGGCC CGTCTTCGAG GGCAGGGTCG AGCTCATGGC	180
AGACCTTGCT GCCAGCCCAC CAGCTATCTG GATGTGACCT TCCTTGATGA CCACCACCAT	240
TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A	291.

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG	60
GTCATCAAGG AAGGTACACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC	120
TCGACCCCTGC CCTCGAACAG GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG C	291.

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met	Ala	Ala	Gly	Arg	Leu	Arg	Ile	Leu	Phe	Leu	Leu	Leu	Leu	Ser	Leu	
1					5				10						15	
His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala																
					20				25					30		
Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys																
					35				40					45		
Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg Ala Leu Pro Gly																
					50				55					60		
Leu Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu																
					65				70					75		80
Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser																
					85				90					95		
Cys Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu																
					100				105					110		
Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser																
					115				120					125		
Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu																
					130				135					140		
Pro Gln Leu Ser Ala Ala Cys Gly Cys Gly Gly																
					145				150					155		

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met	Ala	Ala	Gly	Arg	Leu	Arg	Ile	Leu	Phe	Leu	Leu	Leu	Ser	Leu	
1					5				10					15	
His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala															
					20				25					30	

Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys
 35 40 45

Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ala Leu Pro Gly Leu Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15

Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr
 20 25 30

Cys Ala Gly Ser Cys Pro Gln Glu Val Arg Thr Gln His Ser Leu Val
 35 40 45

Leu Ala Arg Leu Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60

Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His
 65 70 75 80

Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCCTGT CCGTGGCAGA GCTAGGCCTG 60

GGCTACGCCT CAGAGGAGAA GGTCACTCTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT 120

GCCCCGCACCC AGCATGGCCT GGCCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGT 180

GGGCCCTGCT GCCGGCCCAC TCGCTACACC GACGTGGCCT TCCCTCGATGA CGGCCACCGC 240

TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A 291

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

TCAGGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG	60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CACCGTGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C	291

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCCTGT CCGTGGCAGA GCTAGGCCTG	60
GGCTACGCCT CAGAGGAGAA GGTACATCTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT	120
GCCCCCACCC AGCATGGCCT GGCCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGC	180
GGGCCCTGCT GCCGGCCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC	240
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCAGCT GTGGTGGCTG A	291

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TCAGGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG	60
--	----

GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAAGATGAC CTTCTCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C	291

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

ATGGCCGTAG GGAAGTTCTCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGCC CCGATGCCCG TGCGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG	120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGC ACCCACCGCC CCCTTGCCCCG CCTGCGCCGA	180
GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCCTGT CCGTGGCAGA GCTAGGCCTG	240
GGCTACGCCT CAGAGGAGAA GGTCACTTC CGCTACTGCG CGGGCAGCTG CCCCCGTGGT	300
GCCCGCACCC AGCATGGCCT GGCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGT	360
GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC	420
TGGCAGCGGC TGCCCCAGCT CTGGCGCT GCCTGCGGCT GTGGTGGCTG A	471

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG	60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CACCGTGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAAGATGAC CTTCTCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGGCGCAG	300
GCGGGCAAGG GGGCGGTGGG TGCCCAAGCCA GGTCCCTCCA GCCTTGCCA CCTGTTCAAGA	360

CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCCAG	420
CTGCAGGGAC AGGAGCAGCA GAGAGCCCAG CAGGAACTTC CCTACGGCCA T	471

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ATGGCCGTAG GGAAGTTCTT CCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGCC CCGATGCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG	120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGC ACCCACCGCC CCCTTGCCCG CCTGCGCCGA	180
GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCCTGT CCGTGGCAGA GCTAGGCCTG	240
GGCTACGCCT CAGAGGGAGAA GGTCACTTTC CGCTACTGCG CGGGCAGCTG CCCCCGTGGT	300
GCCCGCACCC AGCATGGCCT GGCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGC	360
GGGCCCTGCT GCCGGCCAC TCGCTACACCGACGTGGCCT TCCTCGATGA CCGCCACCGC	420
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCAGCT GTGGTGGCTG A	471

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TCAGGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGC AGCCGCTGCC AGCGGTGGCG	60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCCTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGGCGCAG	300
GCAGGGCAAGG GGGCGGTGGG TGCCCAGCCA GGTCCCTCCA GCCTTGCCA CCTGTTCAGA	360
CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCCAG	420
CTGCAGGGAC AGGAGCAGCA GGGAGCCCAG CAGGAACTTC CCTACGGCCA T	471

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATGGCCGTAG GGAAGTCCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGC	69

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GCCCCAGCCC TGTCCCAGCT GCAGGGACAG GAGCAGCAGA GAGCCCAGCA GGAACTTCCC	60
TACGGCCAT	69

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATGGCCGTAG GGAAGTCCT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGC	69

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GCCCCAGCCC TGTCCCAGCT GCAGGGACAG GAGCAGCAGG GAGCCCAGCA GGAACCTCCC	60
TACGGGCCAT	69

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCCGATGCC C GTGGGGTTCC CGTGGCCGAT GGAGAGTTCT CGTCTGAACA GGTGGCAAAG	60
GCTGGAGGGA CCTGGCTGGG CACCCACCGC CCCCTTGCCC GCCTGCGCCG A	111

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC	60
CTGTTCAAGAC GAGAACTCTC CATCGGCCAC GGGAACCCCA CGGGCATCGG G	111

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ATGGCCGTAG GGAAGTTCT CTGGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGCC CCGATGCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG	120

GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACCGCC CCCTTGCCCC CCTGCGCCGA 180

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC 60

CTGTTCAGAC GAGAACTCTC CATCGGCCAC GGGAACCCCA CGGGCATCGG GGCCCCAGCC 120

CTGTCCCAGC TGCAGGGACA GGAGCAGCAG AGAGCCAGC AGGAACTTCC CTACGGCCAT 180

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ATGGCCGTAG GGAAGTCCT GCTGGGCTCC CTGCTGCTCC TGTCCTGCA GCTGGGACAG 60

GGCTGGGCC CCGATGCCCG TGGGGTCCCG GTGGCCGATG GAGAGTTCTC GTCTGAACAG 120

GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACCGCC CCCTTGCCCC CCTGCGCCGA 180

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC 60

CTGTTCAGAC GAGAACTCTC CATCGGCCAC GGGAACCCCA CGGGCATCGG GGCCCCAGCC 120

CTGTCCCAGC TGCAGGGACA GGAGCAGCAG GGAGCCAGC AGGAACTTCC CTACGGCCAT 180

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Met	Ala	Val	Gly	Lys	Phe	Leu	Leu	Gly	Ser	Leu	Leu	Leu	Leu	Ser	Leu
1															15
Gln	Leu	Gly	Gln	Gly	Trp	Gly	Pro	Asp	Ala	Arg	Gly	Val	Pro	Val	Ala
															30
Asp	Gly	Glu	Phe	Ser	Ser	Glu	Gln	Val	Ala	Lys	Ala	Gly	Gly	Thr	Trp
															45
Leu	Gly	Thr	His	Arg	Pro	Leu	Ala	Arg	Leu	Arg	Arg	Ala	Leu	Ser	Gly
															60
Pro	Cys	Gln	Leu	Trp	Ser	Leu	Thr	Leu	Ser	Val	Ala	Glu	Leu	Gly	Leu
															80
Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser
															95
Cys	Pro	Arg	Gly	Ala	Arg	Thr	Gln	His	Gly	Leu	Ala	Leu	Arg	Leu	
															110
Gln	Gly	Gln	Gly	Arg	Ala	His	Gly	Gly	Pro	Cys	Cys	Arg	Pro	Thr	Arg
															125
Tyr	Thr	Asp	Val	Ala	Phe	Leu	Asp	Asp	Arg	His	Arg	Trp	Gln	Arg	Leu
															140
Pro	Gln	Leu	Ser	Ala	Ala	Cys	Gly	Cys	Gly						
															155

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met	Ala	Val	Gly	Lys	Phe	Leu	Leu	Gly	Ser	Leu	Leu	Leu	Ser	Leu	
1														15	
Gln	Leu	Gly	Gln	Gly	Trp	Gly	Pro	Asp	Ala	Arg	Gly	Val	Pro	Val	Ala
															30

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
 35 40 45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Ser Leu
 1 5 10 15

Gln Leu Gly Gln Gly Trp Gly
 20

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Pro Asp Ala Arg Gly Val Pro Val Ala Asp Gly Glu Phe Ser Ser Glu
 1 5 10 15

Gln Val Ala Lys Ala Gly Gly Thr Trp Leu Gly Thr His Arg Pro Leu
 20 25 30

Ala Arg Leu Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Ala	Leu	Ser	Gly	Pro	Cys	Gln	Leu	Trp	Ser	Leu	Thr	Leu	Ser	Val	Ala
1														15	
Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr
														30	
Cys	Ala	Gly	Ser	Cys	Pro	Arg	Gly	Ala	Arg	Thr	Gln	His	Gly	Leu	Ala
														45	
Leu	Ala	Arg	Leu	Gln	Gly	Gln	Gly	Arg	Ala	His	Gly	Gly	Pro	Cys	Cys
														60	
Arg	Pro	Thr	Arg	Tyr	Thr	Asp	Val	Ala	Phe	Leu	Asp	Asp	Arg	His	Arg
														80	
Trp	Gln	Arg	Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly
														95	

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGCCAGCTGT	GGAGCCTGAC	CCTGTCCGTG	GCAGAGCTAG	GCCTGGGCTA	CGCCTCAGAG	60
GAGAACGGTCA	TCTTCCGCTA	CTGCGCCGGC	AGGTGCCCCC	GTGGTGCCCG	CACCCAGCAT	120
GGCCTGGCGC	TGGCCCGGCT	GCAGGGCCAG	GCCCGAGCCC	ACGGTGGGCC	CTGCTGCCGG	180
CCCACTCGCT	ACACCGACGT	GGCCTTCCTC	GATGACCGCC	ACCGCTGGCA	GCGGCTGCC	240
CAGCTCTCGG	CGGCTGCCTG	CGGCTGT				267

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Cys	Gln	Leu	Trp	Ser	Leu	Thr	Leu	Ser	Val	Ala	Glu	Leu	Gly	Leu	Gly
1														15	
Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys
														30	
Pro	Arg	Gly	Ala	Arg	Thr	Gln	His	Gly	Leu	Ala	Leu	Ala	Arg	Leu	Gln
														45	

Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg Tyr
 50 55 60
 Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Ala Leu Ser Gly Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GTSASYGASY TGGGYCTGGG CTAY

24

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

TTYMGSTACT GCRSMGGCKC YTGC

24

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

RWAGGCSRTS GGKCKGCARC AKGS

24

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

MKCRTCYARR AASGACASST C

21

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

CGGCTTGTGA CCGAGCTGGG CCTGGGCTAC GCCTCAGAGG AGAAGGTCAT CTTCCGCTAC

60

TGCGCCGGCA GCTGCCCGG TGGTGCCCGC ACCCAGCATG GCCTGGCGCT GGCCCGGCTG

120

CAGGGCCAGG GCCGAGCCA CGGGGGCCC TGCTGCCGCC CCATGGCC

168

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAGGAGAAGG TCATCTTCCG

20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GCCGTGGGCT CGGCCCTGGC

20

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

AGAGGAGAAG GTCATCTTCC GCTA

24

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CTCGGCCCTG GCCCTGCAGC

20

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGCAGCCGGG CCAGCGCCAG

20

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CGCGGATCCA TGCCTGGATT CGAGGGTGCA G

31

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CGCGGATCCA TGGCCGTAGG GAAGTTCCCTG C

31

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCGC CACCACAGCC GCAGGCAGCC

60

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCTC GAGGAAGGCC ACGTCGGTG

59

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TCAGGCCACCA CAGCCGCAGG CAGCC

25